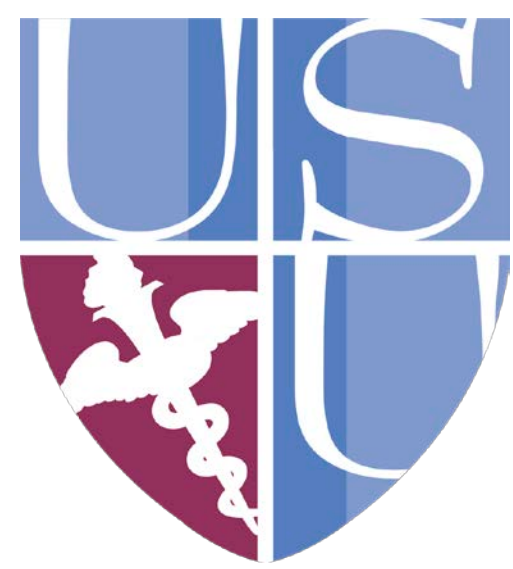


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# USE OF HUMAN ENTERIC VIRUS DETECTION AND GROUNDWATER GEOCHEMISTRY TO CHARACTERIZE THE RISK OF PUBLIC SUPPLY WELL CONTAMINATION



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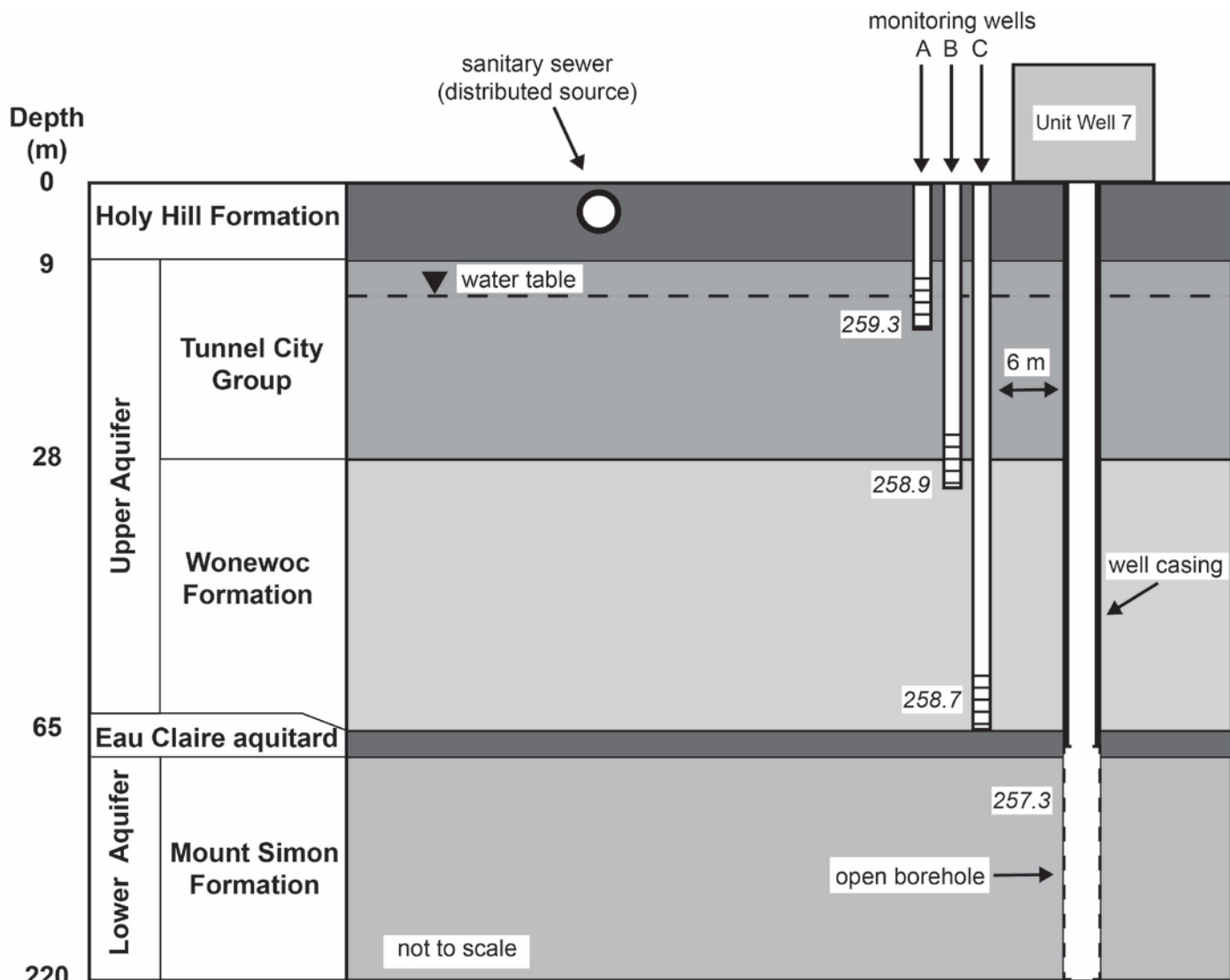
## Abstract

Approximately one third of the U.S. population uses public supply wells as their drinking water source. Recently a greater focus has been placed on assessing the risk of contaminants, to include human enteric viruses, entering these wells. Determining the travel time for near-surface contaminants to reach deep wells is important because these viruses are only infectious in the groundwater environment for 1-2 years. This research utilized time-sequenced sampling of groundwater at discrete depths to detect human enteric viruses and geochemical parameters. The goal was to determine the factors by which a well is likely to become contaminated by sewer-derived wastewater. Virus sampling required pumping 800-1,000 L of groundwater through electropositive glass wool filters. Real time quantitative reverse transcription-polymerase chain reaction (qRT-PCR) methods were used to determine the virus genome concentrations for adenovirus, rotavirus, enterovirus, hepatitis A virus, and norovirus genogroups I and II. Geochemical analyses included major ions, electrical conductivity, temperature, and pH.

Microbiological and chemical wastewater indicators were found at various depths in the aquifer system and in the well. These data improve the understanding of how wastewater may rapidly travel from a sanitary sewer into a deep confined aquifer and reach a public supply well. The combination of geochemical and virus data builds support for a conclusion that bedrock fractures create the preferential flow pathways that allow contaminants to rapidly reach a deep well. These types of fractures may also be present in other aquifer systems but their contribution to groundwater flow and transport may not be appreciated.

## Introduction

There are substantial public health risks associated with virus contamination of drinking water supplies and recent research has demonstrated a link between viruses in non-disinfected public supply wells (PSW) and the incidence of acute gastrointestinal illness (Borchardt et al. 2012). Previous research in Madison, Wisconsin (Borchardt et al. 2007) detected human enteric viruses in several PSWs but the upper aquifer and potential transport pathways were not investigated. This work used sampling of chemical and microbiological indicators of wastewater contaminants to identify the most likely preferential flow pathways in a fractured siliciclastic aquifer system near a Madison Unit Well 7 (UW-7), depicted in Figure 1.



**Figure 1.** Cross section of field site with location of monitoring wells with respect to the unit well. Numbers next to each monitoring well screen and the Unit Well 7 borehole are hydraulic head elevations (in meters) from May 2012 while the aquifer system was at steady state during well maintenance.

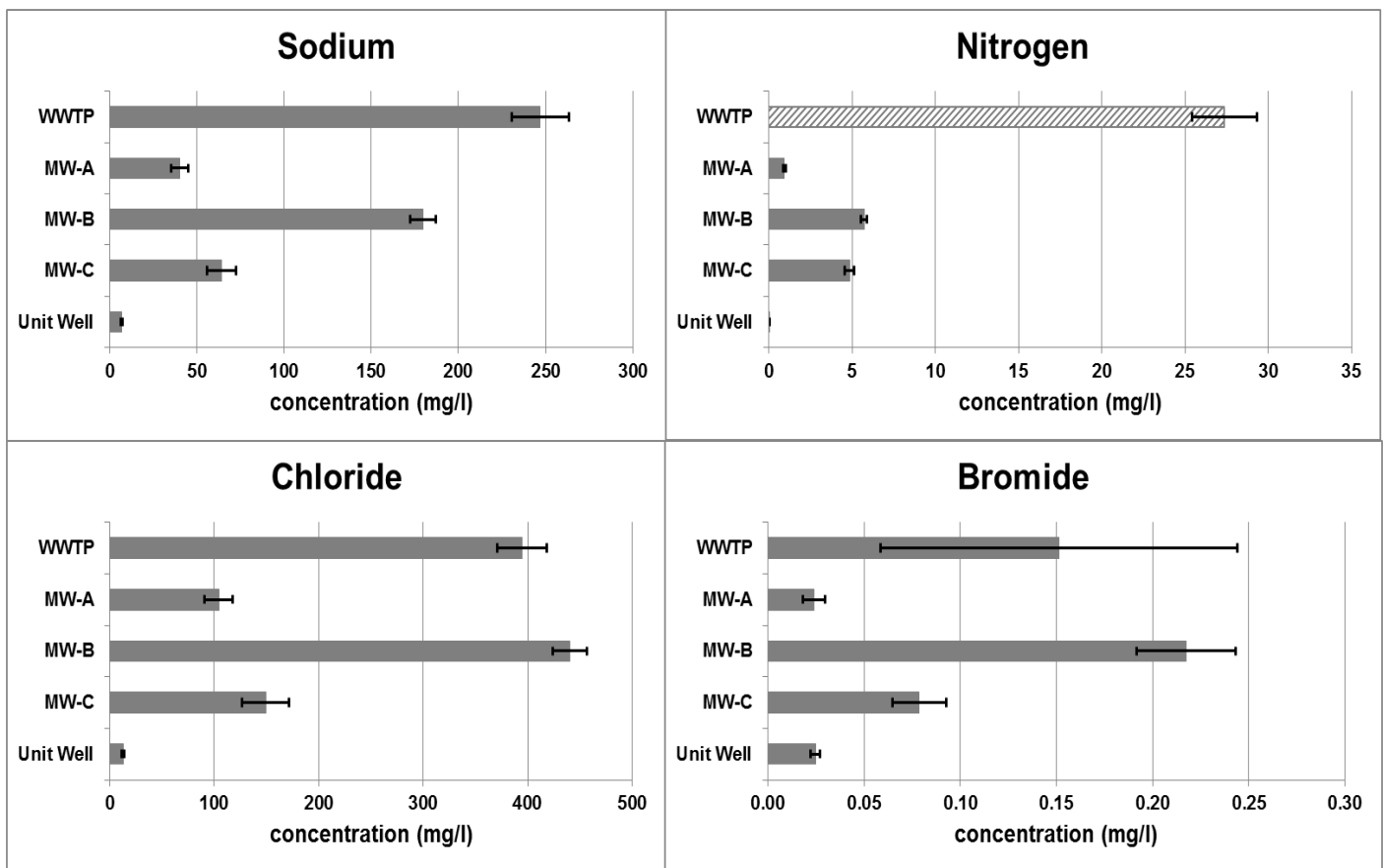
## Methods

The constituents sampled included human enteric virus genomes detected in earlier Madison projects (Borchardt et al. 2007) and chemical wastewater indicators. In order to address the questions related to rapid transport of wastewater contaminants from the near surface to a PSW, a sampling strategy that involved both spatial and temporal aspects of the problem was required (Table 1).

Spatial resolution was achieved by sampling at multiple points between the most likely source (sewer) and UW-7. Characterization of the likely virus source was conducted by sampling wastewater from the sanitary sewer near UW-7 and also influent to the wastewater treatment plant (WWTP). The upper aquifer was sampled from three nested monitoring wells (Figure 1) that were open to the water table (MW-A), a short interval at a depth approximately halfway between the water table and the bottom of the upper aquifer (MW-B), and at the bottom of the upper aquifer (MW-C). The lower aquifer was sampled directly from UW-7 during normal pumping.

Year	Start Date	End Date	Frequency	Sampling Rounds	Total Samples	Locations Sampled
2010	13 May	21 Jul	2x/month	6	30	Sewer, MW-A, MW-B, UW-7, WWTP
2011	24 Feb	24 Feb	single event	1	3	MW-A, MW-B, UW-7
2012	4 Jan	16 May	2x/month	10	49	MW-A, MW-B, MW-C, UW-7, WWTP

**Table 1.** Information on sampling rounds described in this study.



**Figure 2.** Average values for selected constituents from 2012 samples with error bars indicating one standard deviation from the mean. Nitrogen values are reported as NH<sub>3</sub>-N for wastewater treatment plant samples and NO<sub>3</sub>-N for all others.

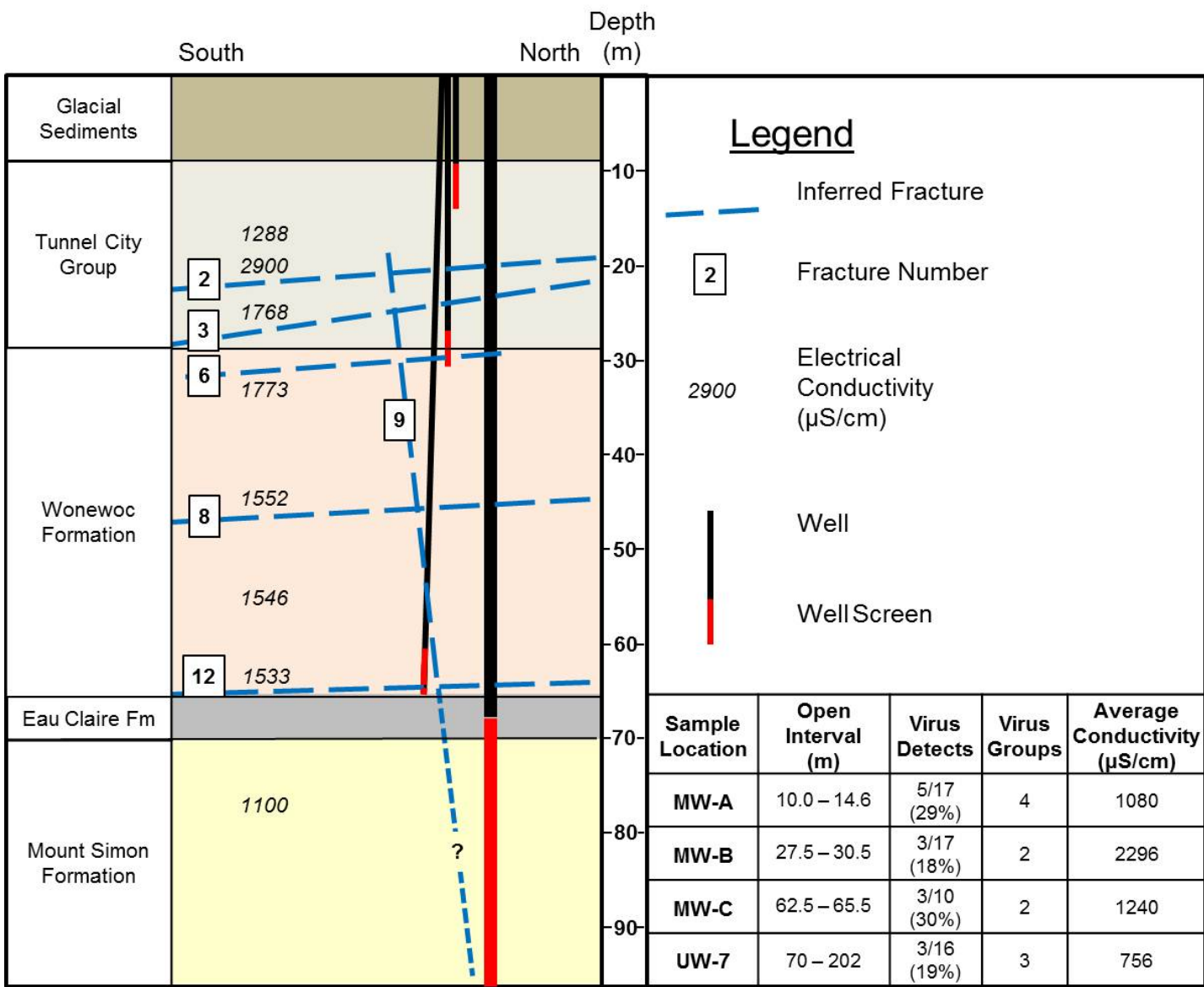
Sampling Week		4-Jan-12	25-Jan-12	8-Feb-12	22-Feb-12	7-Mar-12	21-Mar-12	4-Apr-12	18-Apr-12	2-May-12	16-May-12
WWTP	Adenovirus A	3.8	4.0	3.9	4.1	3.9	3.7	4.2	4.0	4.0	
	Adenovirus B	3.1									
	Adenovirus C,D,F	4.7	4.4	4.8	4.8	4.2	4.3	3.9	3.9	4.3	3.5
	Enterovirus	4.3	4.1	4.0	4.1	3.6	4.8	4.7		4.7	4.8
	G1 Norovirus	4.9	4.9	5.0	5.0	5.0	4.6	4.7	5.3	4.6	4.9
MW-A	Adenovirus A										
	Adenovirus B										
	Adenovirus C,D,F						-0.3				
	Enterovirus					0.01					
	G1 Norovirus		0.7			0.8					
MW-B	Adenovirus A										
	Adenovirus B										
	Adenovirus C,D,F										
	Enterovirus										
	G1 Norovirus							-0.4			
MW-C	Adenovirus A										
	Adenovirus B										
	Adenovirus C,D,F								-1.0		
	Enterovirus			-0.5	-0.2						
	G1 Norovirus										
Unit Well	Adenovirus A				-1.5						No Sample
	Adenovirus B										
	Adenovirus C,D,F										
	Enterovirus										
	G1 Norovirus		0.7								
Precipitation (cm)	14 day total	1.3	3.1	0.2	0.6	3.2	2.3	3.2	1.8	5.4	3.5
	Max daily	2.5	5.1	5.1	2.5	7.6	1.1	2.0	0.94	2.5	2.6

Viruses were detected throughout the upper aquifer and in UW-7 during the 2012 sampling (Table 2). Virus genome groups in the groundwater matched those in the wastewater but at much lower concentrations and were not consistently detected over time. A lack of substantial recharge events during this period hampered efforts to correlate virus detection with recharge.

**Table 2.** Results of 2012 virus sampling reported as log concentration (gc/l). Precipitation data are for the total over the 14 days before sampling and the maximum daily value during that period. Blue shaded precipitation values are for snow melt.

## Discussion

A conceptual model (Figure 3) was created to evaluate preferential flow pathways in terms of chemical and microbial wastewater indicators. This model is based on the fracture flow conceptual model described by Gellasch et al. (2013) but modified to include electrical conductivity and virus data. The conductivity data suggest that fractures are the most likely flow pathway for wastewater contaminants. Mixing of groundwater from Fractures 2 and 6 in almost equal proportions would explain the observed values in MW-B. The values in MW-C can be explained by mixing one part Fracture 12 groundwater with two parts Mount Simon groundwater as measured at the top of the UW-7 borehole during logging.



**Figure 3.** Conceptual model of the Unit Well 7 site based on fracture, virus, and chemistry data. The lower 100+ m of the Mount Simon Formation and Unit Well 7 are not shown. For location of wells see Figure 1.

## Conclusion

Time sequenced sampling for human enteric viruses and geochemical parameters is a useful tool for characterizing transport within a fractured aquifer system. The microbiological and chemical data from wastewater and groundwater samples improved the understanding of how near surface wastewater may travel into a deep confined aquifer and reach a public supply well. Fractures are the most likely preferential flow pathways at this site that allow wastewater contaminants to reach the lower aquifer.

## References

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